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Result
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Listing first 45 summaries
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        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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p15590 zea mays (m
p43238 arachis hyp
p43237 arachis hyp
p43237 arachis max
p11827 glycine max
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p028438 vicia faba
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p10562 canavalia v
p13919 pisum sativ
p02853 phaseolus v
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VICILIN GC72-A

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                                                         PFAM; PF00546; Seedstore_7s;
                                                                                                                                       EMBL; M19378; AAA33069.1; PIR; S06398; S06398.
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                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for commodified the statement is not removed.
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SIMILARITY: TO OTHER 7S SEED STORAGE PROTEINS (PHASEOLIN, VICILIN CONVICILIN, CONGLYCININ, ETC.).
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SEQUENCE
                                                                           Zea mays (Maize).
Zea mays (Maize).
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Embryophyta; Poaceae; Zea.
      Plant Physiol.
                    by the Glb1 gene.
                                        STRAIN=CV. INBRED L. Belanger F.C., Kriz
                                                                SEQUENCE FROM N.A.
                            Molecular characterization of
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                                                   INBRED LINE VA26,
         91:636-643(1989)
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Pred. No. 5.9e-
21; Mismatches
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SQ TETT
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Best Local Similarity
Matches 210; Conser
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SEQUENCE
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Seed storage protein; Signal.
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PTM: THREE PROTEIN-PROCESSING STEPS OCCUR IN THE FORMATION OF MATURE PROTEIN FROM THE PRIMARY TRANSLATION PRODUCT.

POLYMORPHISM: THE THREE MOST COMMONLY OCCURRING GLB1 ALLELES FOR THE DESIGNATION L, I, AND S FOR LARGE, INTERMEDIATE, AND SMALL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: TO OTHER 7S SEED STORAGE PROTEINS (PHASEOLIN, VICILIN, CONVICILIN, CONGLYCININ, ETC.).
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SSGNENULLLFAFGINAQNNHENFLAGRERNVLQQIEPQAMELAFAASRKEVEELFNSQDE: | : | : | : | | : | | : | | : | | : | | : | | : |
                                                                                                                                                                                                                       INRDNNERLHIAKFLQTISTPGQYKEFFPAGGQNPEPYLSTFSKEILEAALNTQTERLRG
                                                       HRQSQGGESERERGKGRRSEEEEESSEEQEEVGQGYHTIRARLSPGTAFVVPAGHPFVAV
                                                                            HLSGRHG----GRGGGKRHEEEEEEVHYEQ-------VRARLSKREAIVVLAGHPVVFV
                                                                                                                            QHGQLYEADARSFHDLAEHDVSVSFANITAGSMSAPLYNTRSFKIAYVPNGKGYAEIVCP
                                                                                                                                                                                                                                                                                                                                                                                                                                    QRGGSGRYEEGEEKQSD-NPYYFDERSLSTRFRTEEGHISVLENFYGRSKLLRALKNYRL::||:||:||:||:::||:
                                                                                                                                                               KYGQAYEVKPEDYRQLQDMDVSVFIANITQGSMMGPFFNTRSTKVVVVASGEADVEMACP 485
                                                                                                                                                                                                LFGRHGQDKGIIVRATEEQTRELRRHASEGGHGPHWPLPPFGE-SRGPYSLLDQRPSIAN
                                                                                                                                                                                                                                                                       ANTDGRKKLVITKILHTISVPGEFQFFFGPGGRNPESFLSSFSKSIQRAAYKTSSDRLER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   s requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
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Best Local S
Matches 210
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J. Clin. Invest. 96:1715-1721(1995).
-I- SIMILARITY: TO 7S SEED STORAGE PROTEINS (PHACONVICILIN, CONGLYCININ, ETC.).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AH12_ARAHY
P43238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; eurosids I; Magnoliophyta; edicottyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Arachis
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01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
ALLERGEN ARA H 1, CLONE P41B (ARA H I).
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DFFPASSRDQSSYLQGFSRNTLEAAFNAEFNEIRRVLLEENAGGEQEERGQRRWSTRSSE 359
                                                                                GGRGALKMIHRDNRESYNLECGDVIRIPAGTTFYLINRDNNERLHIAKFLQTISTPGQYK 335
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                              EFFPAGGQNPEPYLSTFSKEILEAALNTQTERLRGVL-----
                                                               QGQATVTVANGNNRKSFNLDEGHALRIPSGFISYILNRHDNQNLRVAKISMPVNTPGQFE 299
                                                                                                                               RRFSTRYGNONGRIRVLORFDORSROFONLONHRIVOIEAKPNTLVLPKHADADNILVIO
                                                                                                                                                                                                -DWRQPREDW---RRPSHQQPRKIRPEGREGE----QEWGTPGSHVREETSRNNPFYFPS
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J. Clin. Invest. 96:1715-1721(1995)
-i- SIMILARITY: TO 7S SEED STORAGE PROTEINS (PHACONVICILIN, CONGLYCININ, ETC.).
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01-NOV-1995 (Rel. 32, Last sequence up
01-NOV-1997 (Rel. 35, Last annotation a
ALLERGEN ARA H 1, CLONE P17 (ARA H 1).
                                                                                                                                                                                                                                                                     EMBL; L38853; AAA60336.1; HSSP; P50477; 1CAW.
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Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;

Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;

Fabales; Fabaceae; Papilionoideae; Arachis.
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01-NOV-1995
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73
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                                                                                                                                                                                                                                                                                                                                                                            European Bioinformatics Institute.
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                             CQKRCQRRETEPRHMQICQQRCERRYEKEKRKQQKRYEEQQREDEEKYEERMKEGD--NK 145
                                                                           SKYDNQEDPQTEC-QQCQRRCRQQESDPRQQQYCQRRCKEICEEEEEYNRQRDPQQQYEQ 87
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                                                          SPYRKTENP---CAQRCLQSC-QQEPDDLKQKACESRCTKL----
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                                                                                                                                       Score 861; DB 1;
Pred. No. 2.1e-46;
GERTRGRQPGDY----
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modified entities
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Sebastiani F.L., Farrel L.B., Schuler
"Complete sequence of a cDNA of alpha
                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papillonoideae; Glycine.
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01-APN-1990 (Rel. 14, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
BETA-CONGLYCININ, ALPHA CHAIN PRECURSOR.
                                                     the
                                                                                                                                                                                                                                                                    Plant Mol. Biol. - I - FUNCTION: SE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Glycine max (Soybean).
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                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                European Bioinformatics Institute. The by non-profit institutions as long ified and this statement is not removed
                                                                                                                                                                                          CARBON AND NITROGEN SOURCE FOR THE DEVELOPING SEEDLING. SUBUNIT: THE ALPHA'-, ALPHA-, AND BETA-SUBUNITS ASSOCIATE VARIOUS COMBINATIONS TO FORM TRIMERIC PROTEINS.
                                                                                                                      SIMILARITY: TO OTHER 7S SEED CONVICTLIN, CONGLYCININ, ETC.
                                                                                                                                                         VACUOLAR PROTEIN BODIES.
                                                                                                                                                                             SUBCELLULAR LOCATION: EMBRYO AXIS,
                                                                                                                                                                                                                                            TO MOI. BIOI. 15:197-201(1990).
FUNCTION: SEED STORAGE PROTEIN. ACCUMULATES DURING SEED DEVELOPMENT AND IS HYDROLYZED AFTER GERMINATION TO PROVIDE
                                                                                                                                                                                                                                                                                                       Lycinin
                                                                    SWISS-PROT entry is copyright. It is produced through a collaboration sen the Swiss Institute of Bioinformatics and the EMBL outstation -
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Glycine max
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INTERPRO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=86250867; PubMed=3013879;
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                                                                                                                                                                                                                                                               Local Similarity
nes 205; Conser
                                                                                                                                                                                                                                                                                                          Match
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SUBUNIT: THE ALPHA'-, ALPHA-, AND BETA-SUBUNITS ASSOCIATE VARIOUS COMBINATIONS TO FORM TRIMERIC PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CONVICILIN, CONGLYCININ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BODIES.
SIMILARITY: TO OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION: COTYLEDONARY MEMBRANE-BOUND VACUOLAR PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       B24810; B24810.
; P02853; 2PHL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SWISS-PROT entry is copyright. It is produced through a collable of the Swiss Institute of Bioinformatics and the EMBL outst
European Bioinformatics Institute. There are no restrictions
by non-profit institutions as long as its content is in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                glycosylated seed storage proteins caris. Structural homologies of genes iol. Chem. 261:9228-9238(1986).
                                                                               HPERERQQHGEKEEDEGEQPRPFPFPRPR--QPHQEEEHEQKEEHEWHRKEEKHGGKGSE
                                                                                                                           DPQQQYEQCQKRCQRRETEPRHMQICQQRCERRYEKEKRKQQKRYEEQQRED-----E
                                                                                                                                                                                                               WSKYDNQEDPQTECQQCQRRCRQQESDPRQQQYCQRRCKEI-CEEEEEYN-----RQR
EEQDER - - EHPRPHQPHQKEEE - - - KH - EWQHKQEKHQGKESEEEEEDQDEDEEQDKESQ
                                    EKYEERMKEGDNKRDPQQREYEDCRRHCEQQEPRLQYQCQRRCQEQQRQ-HGRGGDLMNP
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Conservative 141;
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N-LINKED (GLCNAC. ..) (PC
N-LINKED (GLCNAC. ..) (PC
P -> L (IN REF. 2).
M -> V (IN REF. 2).
S -> T (IN REF. 2).
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                                                                                                                                                                                                                                                          Score 854.5; DB 1;
Pred. No. 5.6e-46;
1; Mismatches 215;

    Glycoprotein; Multigene family.

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P13915;
                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-CV. FELTHAM FIRST;
MEDITINE-88356208; PubMed=3415641;
Bown D., Ellis T.H.N., Gatehouse J.A.;
The sequence of a gene encoding convicilin from pea
L.) shows that convicilin differs from vicilin by an
                          EMBL; X06398; CAA29695.1;
PIR; S00566; S00566.
HSSP; P02853; 2PHL.
                                                                                                                                            or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Biochem.
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Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
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01-JAN-1990 (Rel. 13, Last sequence update)
01-AUG-1990 (Rel. 15, Last annotation updat
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chem. J. 251:717-726(1988).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   insertion
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                                                                                                                                                                                                                                                                                                                                                                                                           VICILIN
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Matches
                                                                                                                     SBP_SOYBN STAN
Q04672;
Q1-JUN-1994 (Rel. 2
Q1-JUN-1994 (Rel. 2
Q1-JUN-1994 (Rel. 2
SUCROSE-BINDING PRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PFAM; PF00546; Seedstore_7s; 1.
Seed storage protein; Multigene
SIGNAL 1 28
                                                                Glycine max (Soybean).

Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
                          SEQUENCE FROM N.A., AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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MEDLINE=93104680;
            TISSUE=EMBRYO
                                                     Fabales;
                                                                                                                                                                                                                                                             545
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                                                                                                                                                                                                                                                                                     FPG-PRQHQQQSPRSTKQQQPLVSILD
                                                                                                                                                                                                                                                                                                                               NENLLLFAFGINAQNNHENFLAGRERNVLQQIEPQAMELAFAASRKEVEELFNSQDESIF
                                                                                                                                                                                                                                                                                                                                                                                                                                       YSNKYGQAYEVKPE-DYRQLQDMDVSVFIANITQGSMMGPFFNTRSTKVVVVASGEADVE 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QLRDRKRTQQGEERD-AIIKVSREQIEELRKLAKSSS----KKSLPSEFEPFNLRSHKPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  storage protein; Multigene family, Signal.
                                                                                                                                                                                                                                                            ASAEPEQKEEESQR---KRSPLSSVLD
                                                                                                                                                                                                                                                                                                                                                                     TL-----
                                                                                                                                                                                                                                                                                                                                                                                               MACPHLSGRHGGRGGGKRHEEEEEVHYE----
                                                                                                                                                                                                                                                                                                                                                                                                                        YSNKFGKLFEITPEKKYPQLQDLDILVSCVEINKGALMLPHYNSRAIVVLLVNEGKGNLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VDFVIPVNRPGKFEAF--GLSENKNQYLRGFSKNILEASLNTKYETIEKVLLEEQEKKPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AKFLQTISTPGQYKEFFPAGGQNPEPYLSTFSKEILEAALNTQTERLRGVL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SESQEHRNPFLFKSNKFLTLFENENGHIRRLQRFDKRSDLFENLQNYRLVEYRAKPHTIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GEEKQSDNPYYFDERSLSTRFRTEEGHISVLENFYGRSKLLRALKNYRLVLLEANPNAFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SQRREDPEER-------ARLRHREER--TKRDRRH------QREGEEEERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GDNKRDPQQREYEDCRRHCEQQEPRLQYQCQRRCQEQQRQHGRGGDLMNPQRGGSGRYEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E----KEEHE------EEKQKYRYQREKKEQKEVQPGRERWEREEDEEQVEEEWRG 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EQCQKRCQRRETEPRHMQICQQRCERRYEKEKRKQQK----RYEEQQREDEEKYEERMKE 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VTYANYD--EGSETRVPGQRERGRQ-------EGEKEEKRHGEWRPSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IDWSKYDNQEDPQTECQQCQRRCRQQESDPRQQQYCQRRCKEICEEEEEYNRQRDPQQQY 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ------GQQREGVITRASQEQIRELTRDDSESRRWHIRRGGESSRGPYNLFNKRPL 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          al Similarity
208; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            571 AA;
                                                                                                                                                                                                                                                                                                                -GFGINAKNNQRNFLSGSDDNVISQIENPVKELTFPGSSQEVNRLIKNQKQSHF:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29
                                                                                                                                                                                          STANDARD;

    29, Created)
    29, Last sequence update)
    29, Last annotation updat
    PROTEIN PRECURSOR (SBP).

PubMed=1467654;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         571
                                                     Papilionoideae;
                                                                                                                                                                                                                                                                                                                                                                    GLKNEQQEREDRKERNNEVQRYEARLSPGDVVIIPAGHPVAISASS
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                          SEQUENCE OF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 833; DB
Pred. No. le-44
12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CONVICILIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            749CFBEB2D16D57B CRC64
                                                                                                                                                                                                                                                                                     621
                                                                                                                     (SBP).
                                                  Glycine.
                          30~50
                                                                                                                                                                                          524
                                                                                                                                                                                                                                                                                                                                                                                             -QVRARLSKREAIVVLAGHPVVFVSSG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           193;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     571;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                  486
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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Plant Cell 4:1561-1574(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PFAM; PF00546; Seedstore_7s;
Transport; Sugar transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INTERPRO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; L06038; AAB03894.1; -.
                                                                                                                                                                                           317
                                                                                                                                                                                                                                                         419
                                                                                                                                                                                                                                                                                                                                                                                 359
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SUBSCELLULAR LOCATION: MEMBRANE-ASSOCIATED.
TISSUE SPECIFICITY: ASSOCIATED WITH THE PLASMA MEMBRANE OF
TISSUE SPECIFICITY: ASSOCIATED IN SUCROSE TRANSPORT, INCLUDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEVERAL CELL TYPES ENGAGED IN SUCROSE TRANSPORT, INCLUDING THE MESOPHYLL CELLS OF YOUNG SINK LEAVES, THE COMPANION CELLS OF MATURE PHLOEM AND THE CELLS OF DEVELOPING.

MATURE PHLOEM AND THE CELLS OF DEVELOPING COTYLEDONS.

DEVELOPMENTAL STAGE: IN THE COTYLEDON, EXPRESSION IS NOT DETECTED UNTIL 10 DAYS AFTER FERTILIZATION. BETWEEN 10-19 DAYS AFTER FERTILIZATION. BETWEEN 10-19 DAYS AFTER FERTILIZATION, EXPRESSION INCREASES RAPIDLY BUT DECLINES 20-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DAYS AFTER FERTILIZATION. 30 DAYS AFTER FERTILIZATION, NO EXPRESSION OCCURS. THIS EXPRESSION PATTERN CLOSELY PARALLELS RATE OF SUCROSE UPTAKE IN THE COTYLEDON.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RCKEICEEEEEVNRQRDPQ--QQYEQCQKRCQRRETEPRHMQICQQRCERRYEKEKRKQQ 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JQ1730; JQ1730.
; P50477; 1CAW.
ENLLLFAFGINAQNNHENFLAGRERNVLQQIEPQAMELAF-
                                                                    RGHLQISCPHMS----
                                                                                                                                                                                                                                                                                                             AALQTPKGKLENVFDQQNEGSIFRISREQVRALA-PTKKSSWWPF--GGE-SKPQFNIFS
                                                                                                                                                                                                                                                                                                                                                                                                                                        HIPAGTPLYIVNRDENDKLFLAMLHIPVSVSTPGKFEEFFAPGGRDPESVLSAFSWNVLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RIPAGTTFYLINRDNNERLHIA--KFLQTISTPGQYKEFFPAGGQNPEPYLSTFSKEILE 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LLQGIENERLAILEARAHTEVSPRHEDSEVVEENIKGRAVLGLVSESETEKITLEPGDMI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LLRALKNYRLVLLEANPNAFVLPTHLDADAILLVIGGRGALKMIHRDNRESYNLECGDVI 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KRYEEQQREDEEKYEERMKEGDNKRDPQQREYEDCRRHCEQQEPRLQYQCQRRCQEQQRQ 181
                                                                                                                    EADVEMACPHLSGRHGGRGGKRHEEEEEEVHYEQVRARLSKREAIVVLAGHPVVFVSSGN
                                                                                                                                                                                        KRPTISNGYGRLTEVGPDDDEKSWLQRLNLMLTFTNITQRSMSTIHYNSHATKIALVIDG
                                                                                                                                                                                                                                               KRPLYSNKYGQAYEVKPEDYRQ---LQDMDVSVFIANITQGSMMGPFFNTRSTKVVVVVASG
                                                                                                                                                                                                                                                                                                                                                                          AALNTQTERLRGVLGQQREGVIIRASQEQIRELTRDDSESRRWHIRRGGESSRGPYNLFN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HGRGGDLMNPQRGGSGRYEEGEEKQSDNPYYFDE-RSLSTRFRTEEGHISVLENFYGRSK 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KQIQEETRE-----KKEEESRERE--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KCKETEVEEE-----DPELVTCKHQCQQQQQYTEGDKR----VCLQSCD-RYHRMKQERE 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IPR001113; -.
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524 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              524
60522 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23.9%;
                                                             -SRSSHSKHDKSSP-SYHRISSDLKPGMVFVVPPGHPFVTIASNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --EEQDENPYIFEEDKDFETRVETEGGRIRVLKKFTEKSK 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Signal; Membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 794; DB 1;
Pred. No. 2.5e-42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUCROSE-BINDING PROTEIN. 0251EE90796EF341 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches 176; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 524;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -EEQQEQ 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               THE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Isolation and expression of a pea vicilin cDNA in Saccharomyces cerevisiae."; Biochem. J. 251:857-864(1988).
                                                                                                                                                                                             CHAIN
                                                                                                                                                                                                                    SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X14076; CAA32239.1; -. EMBL; Y00722; CAA68708.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=CV. FELTHAM FIRST;
MEDLINE=88326226; PubMed=3046604;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "The sequence of a pea vicilin
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Eukaryota; Viridiplantae;
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15-JUL-1999 (Rel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gatehouse J.A., Wright D.J.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Plant Mol. Biol. 11:683-695(1988).
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$08505; $08505.
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al Similarity
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                                                                                                                  VICILIN.

V -> L (IN REF. 2).

I -> V (IN REF. 2).

I => D (IN REF. 2).
                   Score 759.5; DB 1
Pred. No. 2.9e-40;
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01-MAY-1992 (Rel. 22, Las
01-NOV-1995 (Rel. 32, Las
01-NOV-1995 (Rel. 32, Las
                                                                                                                                                                                                              PLANT Cell 1:415-425(1989).

-i- FUNCTION: SEED STORAGE PROTEIN. ACCUMULATES DURING SEED DEVELOPMENT AND IS HYDROLYZED AFTER GERMINATION TO PROVIDE CARBON AND NITROGEN SOURCE FOR THE DEVELOPING SEEDLING.
-i- SUBUNIT: THE ALPHA'-, ALPHA-, AND BETA-SUBUNITS ASSOCIATE I VARIOUS COMBINATIONS TO FORM TRIMERIC PROTEINS.
-i- SUBCELLULAR LOCATION: EMBRYO AXIS, AND COTYLEDONARY MEMBRAN VACUOLAR PROTEIN BODIES.
-i- SIMILARITY: TO OTHER 7S SEED STORAGE PROTEINS (PHASEOLIN, VCONVICILIN, CONGLYCININ, ETC.).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Glycine max (Soybean).

Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;

Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;

Fabales; Fabaceae; Papilionoideae; Glycine.
                                                                                                                                                                                      This
                       HSSP;
                                       PIR; JQ0969; FWSYCB.
                                                    EMBL; S44893; AAB23463.1;
                                                                                                   use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See
                                                                                                                                                      the
                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-93005638; PubMed-2562562;
Harada J.J., Barker S.J., Goldberg R.B.;
"Soybean beta-conglycinin genes are clustered in several DNA regions
and are regulated by transcriptional and posttranscriptional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GLCB_SOYBN
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                                                                                       send an email to license@isb-sib.ch).
                                                                                                                                     European Bioinformatics Institute. The by non-profit institutions as long
                                                                                                                                   SWISS-PROT entry is copyright. It is produced through a collaboration sen the Swiss Institute of Bioinformatics and the EMBL outstation surpean Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
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                     ACC RATE RANGE RAN
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Best Local
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01-AUG-1988 (Rel. (
01-AUG-1988 (Rel. (
01-JAN-1990 (Rel. )
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SEQUENCE
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PROPEP
                                                                                                                                                                                                                                                STRAIN=CV. MINOR;
MEDLINE=88096511;
Weschke W., Baeum
                                                                                                                                                                                                                                                                                                                                                             Magnoliophyta; eudicotyledons; core eudic Fabales; Fabaceae; Papilionoideae; Vicia.
                                                           STRAIN=CV. FRIBO;
MEDLINE=88067789; PubMe
Bassuener R., van Nong
                                                                                                                                                                                                                                                                                                                                                                                                             Vicia faba (Broad bean).
Eukaryota; Viridiplantae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             VICILIN PRECURSOR
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                                          "The
                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                Nucleic Acids
                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                        "Nucleotide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          427
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                uener R., van Nong H., Jung R., Saalbach
primary structure of the predominating
init from field bean seeds (Vicia faba L.
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Baeumlein H., Wobus U
sequence of a field b
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351
50552
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                                                                                                                                                                                                                                                                                                                                                                                   Embryophyta; Tracheophyta; Spermatophyta; dons; core eudicots; Rosidae; eurosids I;
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Pred. No. 1.2e
37; Mismatches
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N-LINKED (GLCNAC. . .) (F
DBD8AA2A0776088B CRC64;
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EMBL; Y00462; CAA68825.1; -
PIR; S06309; S06309.
PIR; A77288; A27288
HSSP; P50477; ICAW
   P02854;
21-JUL-1986
21-JUL-1986
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                                                        VCLB_PEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation between the Swiss Institute. There are no restrictions on its use buropean Bioinformatics Institute. There are no restrictions on its use buropean Bioinformatics Institutions as its content is in no way the swing as its content is in no way the swing as its content is in no way the swing as its content is in no way the swing as its content is in no way the swing as its content is in no way the swing as its content is in no way the swing as its content is in no way the swing as its content is in no way the swing as its content is in no way the swing as its content is in no way the swing as its content is in no way the swing as its content is in no way the swing as its content is in no way the swing as its content is in no way the swing as its content is in no way the swing as its content is in no way the swing as its content is in no way the swing as its content is in no way the swing as its content is in no way the swing as its content is in no way the swing as its content is in no way the swing as its content is in no way the swing as its content is in no way the swing as its content is in no way the swing as its content is in the swing a
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-!- FUNCTION: SEED STORAGE PROTEIN.
-!- SUBCELLULAR LOCATION: COTYLEDONARY
                                                                                                                                               444
                                                                                                                                                                                                                                                                                                                                                         269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  268
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SIMILARITY: CONVICILIN,
                                                                                                                                             ERERGSQEIKDH--LYSIL
                                                                                                                                                                            HQQQSPRSTKQQQPLVSIL
                                                                                                                                                                                                                                                                                                    KFFEITPKRNPQLQDLNIFVNYVEINEGSLLLPHYNSRAIVIVTVNEGKGDFELVGQRNE
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   (Rel. 01, Created) (Rel. 01, Last seq
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                                                      STANDARD;
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257
443
52694
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     sequence
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R -> K (IN REF.

R -> Q (IN REF.
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Pred. No. 2.1e-37;
                                                        PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=92119225; pubMed=1731967; Ng J.D., Stinchcombe T., Ko T.-P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-COTYLEDON;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fabales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NO T.-P., Ng J.D., McPherson A.;
The three-dimensional structure of
  212
                                                                                                         152
                                                                                                                                                         314
                                                                                                                                                                                                                                                                254
                                                                                                                                                                                                                                                                                                                                                                 194 GGSGRYEEGEEKQSDNPYYFDERSLSTRFRTEEGHISVLENFYGRSKLLRALKNYRLVLL
                                                                                                                                                                                                             92
                                                                                                                                                                                                                                                                                                                   32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           J.D., Ko T.-P., McPherson A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        %L; X59467; CAA42075.1; -
$; ICAU; 31-0CT-93.
$; ICAV; 31-0CT-93.
$; ICAW; 31-0CT-93.
$; ICAX; 31-0CT-93.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBUNIT: HOMOTRIMER.
SIMILARITY: TO OTHER 7S SEED STOOMVICTLIN, CONGLYCININ, ETC.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION: SEED STORAGE PROTEIN
                                                                                                                              DNNERLHIAKFLQTISTPGQYKEFFPAGGQNPEPYLSTFSKEILEAALNTQTERL-RGVL 372
QEEQEGVIVKMPKDQIQEISKHAQSSSRKTL---
                                             GQQREGVIIRASQEQIRELTRDDSESRRWHIRRGGESSRGPYNLFNKRPLYSNKYGQAYE
                                                                                                                                                                                                             CSKPNTLLLPHHSDSDLLVLVLEGQAILVLVNPDGRDTYKLDQGDAIKIQAGTPFYLINP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               storage protein; Signal;
                                                                                                   DNNQNLRILKFAITFRRPGTVEDFFLSSTKRLPSYLSAFSKNFLEASYDSPYDEIEQTLL
                                                                                                                                                                                                                                                          EANPNAFVLPTHLDADAILLVIGGRGALKMIHRDNRESYNLECGDVIRIPAGTTFYLINR 313
                                                                                                                                                                                                                                                                                                                GGEAEDESEESRAQNNPYLFRSNKFLTLFKNQHGSLRLLQRFNEDTEKLENLRDYRVLEY 91
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27
445
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33
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                                                                                                                                                                                                                                                                                                                                                                                                                       99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; 3D-structure.
BY SIMILARITY.
CANAVALIN.
                                                                                                                                                                                                                                                                                                                                                                                                                    Score 692.5;
Pred. No. 3.9e
99; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30383C5F83A1E9B7
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No. 3.9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  3.9e-36;
SSQDKPFNLRSRDPIYSNNYGKLYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             bean)
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RESULT 15
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          CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yamauchi D., Nakamura K., Asahi T., Minamikawa T.;

YoNNAs for canavalin and concanavalin A from Canavalia gladiata
seeds. Nucleotide sequence of cDNA for canavalin and RNA blot
analysis of canavalin and concanavalin A mRNAs in developing see
Eur. J. Biochem. 170:515-520(1988).
                                                                                                           Seed
                                                                                                                                                                                                                                                                                                     modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Canavalia gladiata (Sword bean) (Japanese jack bean).
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; S
Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CANAVALIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUL-1989 (Rel.
01-JUL-1989 (Rel.
01-OCT-1996 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P10562;
01-JUL-1989
                                                        CHAIN
                                                                                    SIGNAL
                                                                                                                                                                                                                                EMBL; X06733; CAA29910.1; -. EMBL; X15076; CAA33172.1; -.
                                                                                                                                                                                                                                                                                                                                                                               the European Bioinformatics Institute. Th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic Acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Nucleotide sequence of the canavaline seeds."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=89296493; PubMed=2740227;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=88111636; PubMed=3338449; Yamauchi D., Nakamura K., Asahi T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A., AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fabales;
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                                                                                                                            PFAM; PF00546; Seedstore_7s;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Leic Acids Res. 17:4381-4381(1989).
FUNCTION: SEED STORAGE PROTEIN.
SUBUNIT: HOMOTRIMER.
SIMILARITY: TO OTHER 7S SEED STORAGE
CONVICILIN, CONGLYCININ, ETC.).
                                                                                                                                                                                                      S00281; S00281.
                                                                                                   storage protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RRAHLP 438
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11, Last sequence up
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                                                                                                        Signal.
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            MW;
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       CANAVALIN.
N -> K (IN REF. 2).
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433 RRAHLP 438
                             610 TKQQQP 615
                                                                                                                                                                  194 GGSGRYEEGEEKQSDNPYYFDERSLSTRFRTEEGHISVLENFYGRSKLLRALKNYRLVLL 253
                                                                                                                                 212 QEEQEGVIVKMPKDQIQEISKHAQSSSRKTL----SSQDKPFNLRSRDPIYSNNYGKLYE 267
                                                                                                                                           32 GGEAEDESEESRAQNNPYLFRSNKFLTLFKNQHGSLRLLQRFNEDTEKLENLRDYRVLEY 91
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Search completed: March 1, 2001, 16:16:47 Job time: 427 sec

